



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5       (i) APPLICANT: Chuntharapai, Anon  
                    Kim, Kyung Jin  
                    Love, Richard B.  
                    Lu, Ji
- 10       (ii) TITLE OF INVENTION: Type I Interferon Receptor Antibodies
- (iii) NUMBER OF SEQUENCES: 22
- 15       (iv) CORRESPONDENCE ADDRESS:  
              (A) ADDRESSEE: Genentech, Inc.  
              (B) STREET: 1 DNA Way  
              (C) CITY: South San Francisco  
              (D) STATE: California  
20       (E) COUNTRY: USA  
              (F) ZIP: 94080
- (v) COMPUTER READABLE FORM:  
              (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
25       (B) COMPUTER: IBM PC compatible  
              (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
              (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:  
30       (A) APPLICATION NUMBER:  
              (B) FILING DATE: 07-Apr-1998  
              (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
35       (A) APPLICATION NUMBER: 08/888,140  
              (B) FILING DATE: 03 July 1997
- (viii) ATTORNEY/AGENT INFORMATION:  
40       (A) NAME: Love, Richard B.  
              (B) REGISTRATION NUMBER: 34,659  
              (C) REFERENCE/DOCKET NUMBER: P1039P1
- (ix) TELECOMMUNICATION INFORMATION:  
45       (A) TELEPHONE: 650/225-5530  
              (B) TELEFAX: 650/952-9881
- (2) INFORMATION FOR SEQ ID NO:1:
- (i) SEQUENCE CHARACTERISTICS:  
50       (A) LENGTH: 7 amino acids  
              (B) TYPE: Amino Acid  
              (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg Trp Asn Arg Ser Asp Glu  
1 5 7

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 7 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Trp Asn Ala Ser Ala Ala  
1 5 7

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Glu Glu Ile Lys Leu Arg  
1 5 6

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Ala Ile Ala Leu Ala  
1 5 6

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Ala Glu Lys Glu  
1 5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 5 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Ala Ala Ala Ala  
1 5

10 (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: Amino Acid  
15 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

20 Glu Val His Leu Glu Ala Glu Asp Lys  
1 5 9

(2) INFORMATION FOR SEQ ID NO:8:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 9 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

30 Ala Val Ala Leu Ala Ala Ala Ala Ala  
1 5 9

(2) INFORMATION FOR SEQ ID NO:9:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu Glu Arg Ile Glu  
1 5

45 (2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 5 amino acids  
50 (B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Ala Ala Ile Ala  
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg His Lys Ile Tyr Lys  
1 5 6

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ala Ala Ala Ile Tyr Ala  
1 5 6

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

His Leu Tyr Lys Trp Lys  
1 5 6

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Ala Leu Tyr Ala Trp Ala  
1 5 6

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Glu Ile Lys Phe Asp Thr Glu  
1 5 8

10 (2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: Amino Acid  
15 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

20 Ala Ala Ile Ala Phe Ala Thr Ala  
1 5 8

(2) INFORMATION FOR SEQ ID NO:17:

25 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

30 Glu Arg Lys Ile Ile Glu Lys Lys  
1 5 8

(2) INFORMATION FOR SEQ ID NO:18:

35 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 8 amino acids  
(B) TYPE: Amino Acid  
40 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

45 Ala Ala Ala Ile Ile Ala Ala Ala  
1 5 8

(2) INFORMATION FOR SEQ ID NO:19:

50 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Glu Lys Leu Asn Lys  
1 5 6

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Ala Ala Leu Asn Ala  
1 5 6

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 6741 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAATTCCGTA ACTGGTGGGA TCTGCGGCGG CTCCCAGATG ATGGTCGTCC 50  
TCCTGGGCGC GACGACCCTA GTGCTCGTCG CCGTGGCGCC ATGGGTGTTG 100  
TCCGCAGCCG CAGGTGGAAA AAATCTAAAA TCTCCTCAAA AAGTAGAGGT 150  
CGACATCATA GATGACAACT TTATCCTGAG GTGGAACAGG AGCGATGAGT 200  
CTGTCGGGAA TGTGACTTTT TCATTCGATT ATCAAAAAAC TGGGATGGAT 250  
AATTGGATAA AATTGTCTGG GTGTCAGAAT ATTACTAGTA CCAAATGCAA 300  
CTTTTCTTCA CTCAAGCTGA ATGTTTATGA AGAAATTAAA TTGCGTATAA 350  
GAGCAGAAAA AGAAAACACT TCTTCATGGT ATGAGGTTGA CTCATTTACA 400  
CCATTTGCA AAGCTCAGAT TGGTCCTCCA GAAGTACATT TAGAAGCTGA 450  
AGATAAGGCA ATAGTGATAC ACATCTCTCC TGGAACAAAA GATAGTGTTA 500  
TGTGGGCTTT GGATGGTTTA AGCTTTACAT ATAGCTTACT TATCTGGAAA 550  
AACTCTTCAG GTGTAGAAGA AAGGATTGAA AATATTTATT CCAGACATAA 600  
AATTTATAAA CTCTCACCAG AGACTACTTA TTGTCTAAAA GTTAAAGCAG 650  
CACTACTTAC GTCATGGAAA ATTGGTGTCT ATAGTCCAGT ACATTGTATA 700

AAGACCACAG TTGAAAATGA ACTACCTCCA CCAGAAAATA TAGAAGTCAG 750  
 TGTCCAAAAT CAGAACTATG TTCTTAAATG GGATTATACA TATGCAAACA 800  
 5 TGACCTTTCA AGTTCAGTGG CTCCACGCCT TTTTAAAAAG GAATCCTGGA 850  
 AACCATTTGT ATAAATGGAA ACAAAATACCT GACTGTGAAA ATGTCAAAAC 900  
 TACCCAGTGT GTCTTTCCTC AAAACGTTTT CCAAAAAGGA ATTTACCTTC 950  
 10 TCCGCGTACA AGCATCTGAT GGAAATAACA CATCTTTTGT GTCTGAAGAG 1000  
 ATAAAGTTTG ATACTGAAAT ACAAGCTTTC CTACTTCCTC CAGTCTTTAA 1050  
 15 CATTAGATCC CTTAGTGATT CATTCCATAT CTATATCGGT GCTCCAAAAC 1100  
 AGTCTGGAAC CACGCCTGTG ATCCAGGATT ATCCACTGAT TTATGAAATT 1150  
 ATTTTTTGGG AAAACACTTC AAATGCTGAG AGAAAAATTA TCGAGAAAAA 1200  
 20 AACTGATGTT ACAGTTCCTA ATTTGAAACC ACTGACTGTA TATTGTGTGA 1250  
 AAGCCAGAGC ACACACCATG GATGAAAAGC TGAATAAAAG CAGTGTTTTT 1300  
 25 AGTGACGCTG TATGTGAGAA AACAAAACCA GGAAATGACA AACTCACAC 1350  
 ATGCCACCG TGCCACGAC CTGAACTCCT GGGGGGACCG TCAGTCTTCC 1400  
 TCTTCCCCC AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG 1450  
 30 GTCACATGCG TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT 1500  
 CAACTGGTAC GTGGACGGCG TGGAGGTGCA TAATGCCAAG ACAAGCCGC 1550  
 35 GGGAGGAGCA GTACAACAGC ACGTACCGAG TGGTCAGCGT CCTCACCGTC 1600  
 CTGCACCAGG ACTGGCTGAA TGGCAAGGAG TACAAGTGCA AGGTCTCAA 1650  
 CAAAGCCCTC CCAGCCCCCA TCGAGAAAAC CATCTCCAA GCCAAAGGGC 1700  
 40 AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCCATCCCG GGAAGAGATG 1750  
 ACCAAGAACC AGGTACGCTT GACCTGCCTG GTCAAAGGCT TCTATCCCAG 1800  
 45 CGACATCGCC GTGGAGTGGG AGAGCAATGG GCAGCCGGAG AACAACTACA 1850  
 AGACCACGCC TCCCGTGCTG GACTCCGACG GCTCCTTCTT CCTCTACAGC 1900  
 AAGCTCACCG TGGACAAGAG CAGGTGGCAG CAGGGGAACG TCTTCTCATG 1950  
 50 CTCCGTGATG CATGAGGCTC TGCACAACCA CTACACGCAG AAGAGCCTCT 2000  
 CCCTGTCTCC GGGTAAATGA GTGCGACGGC CCTAGAGTCG ACCTGCAGAA 2050

GCTTAGAACC GAGGGGCCGC CATGGCCCAA CTTGTTTATT GCAGCTTATA 2100  
 ATGGTTACAA ATAAAGCAAT AGCATCACAA ATTTACAAA TAAAGCATTT 2150  
 5 TTTTCACTGC ATTCTAGTTG TGGTTTGTCC AACTCATCA ATGTATCTTA 2200  
 TCATGTCTGG ATCGATCGGG AATTAATTCG GCGCAGCACC ATGGCCTGAA 2250  
 10 ATAACCTCTG AAAGAGGAAC TTGGTTAGGT ACCTTCTGAG GCGGAAAGAA 2300  
 CCAGCTGTGG AATGTGTGTC AGTTAGGGTG TGGAAAGTCC CCAGGCTCCC 2350  
 CAGCAGGCAG AAGTATGCAA AGCATGCATC TCAATTAGTC AGCAACCAGG 2400  
 15 TGTGGAAAGT CCCCAGGCTC CCCAGCAGGC AGAAGTATGC AAAGCATGCA 2450  
 TCTCAATTAG TCAGCAACCA TAGTCCCGCC CCTAACTCCG CCCATCCCGC 2500  
 CCCTAACTCC GCCCAGTTCC GCCCATTCTC CGCCCCATGG CTGACTAATT 2550  
 20 TTTTTTATTT ATGCAGAGGC CGAGGCCGCC TCGGCCTCTG AGCTATTCCA 2600  
 GAAGTAGTGA GGAGGCTTTT TTGGAGGCCT AGGCTTTTGC AAAAAGCTGT 2650  
 25 TAACAGCTTG GCACTGGCCG TCGTTTTACA ACGTCGTGAC TGGGAAAACC 2700  
 CTGGCGTTAC CCAACTTAAT CGCCTTGCAG CACATCCCCC CTTGCCCAGC 2750  
 TGGCGTAATA GCGAAGAGGC CCGCACCGAT CGCCCTTCCC AACAGTTGCG 2800  
 30 TAGCCTGAAT GGCGAATGGC GCCTGATGCG GTATTTTCTC CTTACGCATC 2850  
 TGTGCGGTAT TTCACACCGC ATACGTCAAA GCAACCATAG TACGCGCCCT 2900  
 35 GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG TGGTTACGCG CAGCGTGACC 2950  
 GCTACACTTG CCAGCGCCCT AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC 3000  
 CTTTCTCGCC ACGTTCGCCG GCTTTCCCG TCAAGCTCTA AATCGGGGGC 3050  
 40 TCCCTTTAGG GTTCCGATTT AGTGCTTTAC GGCACCTCGA CCCCACAAAA 3100  
 CTTGATTTGG GTGATGGTTC ACGTAGTGGG CCATCGCCCT GATAGACGGT 3150  
 45 TTTTCGCCCT TTGACGTTGG AGTCCACGTT CTTTAATAGT GGACTCTTGT 3200  
 TCCAACTGG AACAACTC AACCCATCT CGGGCTATTC TTTTGATTTA 3250  
 50 TAAGGGATTT TGCCGATTTT GGCTATTGG TAAAAAATG AGCTGATTTA 3300  
 ACAAAAATTT AACGCGAATT TTAACAAAAT ATTAACGTTT ACAATTTTAT 3350  
 GGTGCACTCT CAGTACAATC TGCTCTGATG CCGCATAGTT AAGCCAATC 3400



CGCTATCGCT ACGTGA CTGG GTCATGGCTG CGCCCCGACA CCCGCCAACA 3450  
 CCCGCTGACG CGCCCTGACG GGCTTGTCTG CTCCCGGCAT CCGCTTACAG 3500  
 5 ACAAGCTGTG ACCGTCTCCG GGAGCTGCAT GTGTCAGAGG TTTTCACCGT 3550  
 CATCACCAGAA ACGCGCGAGG CAGTATTCTT GAAGACGAAA GGGCCTCGTG 3600  
 10 ATACGCCTAT TTTTATAGGT TAATGTCATG ATAATAATGG TTTCTTAGAC 3650  
 GTCAGGTGGC ACTTTTCGGG GAAATGTGCG CGGAACCCCT ATTTGTTTAT 3700  
 TTTTCTAAAT ACATTCAAAT ATGTATCCGC TCATGAGACA ATAACCCTGA 3750  
 15 TAAATGCTTC AATAATATTG AAAAAGGAAG AGTATGAGTA TTCAACA TTT 3800  
 CCGTGTCGCC CTTATTCCCT TTTTTCGGC ATTTTGCCTT CCTGTTTTTG 3850  
 20 CTCACCCAGA AACGCTGGTG AAAGTAAAAG ATGCTGAAGA TCAGTTGGGT 3900  
 GCACGAGTGG GTTACATCGA ACTGGATCTC AACAGCGGTA AGATCCTTGA 3950  
 GAGTTTTTCGC CCCGAAGAAC GTTTTCCAAT GATGAGCACT TTTAAAGTTC 4000  
 25 TGCTATGTGG CGCGGTATTA TCCCGTGATG ACGCCGGGCA AGAGCAACTC 4050  
 GGTGCGCGCA TACACTATTC TCAGAATGAC TTGGTTGAGT ACTCACCAGT 4100  
 30 CACAGAAAAG CATCTTACGG ATGGCATGAC AGTAAGAGAA TTATGCAGTG 4150  
 CTGCCATAAC CATGAGTGAT AACACTGCGG CCAACTTACT TCTGACAACG 4200  
 ATCGGAGGAC CGAAGGAGCT AACCGCTTTT TTGCACAACA TGGGGGATCA 4250  
 35 TGTAAC TCGC CTTGATCGTT GGGAAACCGGA GCTGAATGAA GCCATACCAA 4300  
 ACGACGAGCG TGACACCACG ATGCCAGCAG CAATGGCAAC AACGTTGCGC 4350  
 40 AAATATTA CTGGCGAACT ACTTACTCTA GCTTCCCGGC AACAA TTAAT 4400  
 AGACTGGATG GAGGCGGATA AAGTTGCAGG ACCACTTCTG CGCTCGGCCC 4450  
 TTCCGGCTGG CTGGTTTATT GCTGATAAAT CTGGAGCCGG TGAGCGTGGG 4500  
 45 TCTCGCGGTA TCATTGCAGC ACTGGGGCCA GATGGTAAGC CCTCCCGTAT 4550  
 CGTAGTTATC TACACGACGG GGAGTCAGGC AACTATGGAT GAACGAAATA 4600  
 50 GACAGATCGC TGAGATAGGT GCCTCACTGA TTAAGCATTG GTAAGTGTCA 4650  
 GACCAAGTTT ACTCATATAT ACTTTAGATT GATT TAAAAC TTCATTTTTA 4700  
 ATTTAAAAGG ATCTAGGTGA AGATCCTTTT TGATAATCTC ATGACCAAAA 4750

TCCCTTAACG TGAGTTTTCG TTCCACTGAG CGTCAGACCC CGTAGAAAAG 4800  
 ATCAAAGGAT CTTCTTGAGA TCCTTTTTTT CTGCGCGTAA TCTGCTGCTT 4850  
 5 GCAAACAAAA AAACCACCGC TACCAGCGGT GGTGTGTTG CCGGATCAAG 4900  
 AGCTACCAAC TCTTTTTCCG AAGGTAAGT GCTTCAGCAG AGCGCAGATA 4950  
 10 CCAAATACTG TCCTTCTAGT GTAGCCGTAG TTAGGCCACC ACTTCAAGAA 5000  
 CTCTGTAGCA CCGCCTACAT ACCTCGCTCT GCTAATCCTG TTACCAGTGG 5050  
 CTGCTGCCAG TGGCGATAAG TCGTGTCTTA CCGGGTTGGA CTCAAGACGA 5100  
 15 TAGTTACCGG ATAAGGCGCA GCGGTCGGGC TGAACGGGGG GTTCGTGCAC 5150  
 ACAGCCCAGC TTGGAGCGAA CGACCTACAC CGAACTGAGA TACCTACAGC 5200  
 GTGAGCATTG AGAAAGCGCC ACGCTTCCCG AAGGGAGAAA GGCGGACAGG 5250  
 20 TATCCGGTAA GCGGCAGGGT CGGAACAGGA GAGCGCACGA GGGAGCTTCC 5300  
 AGGGGGAAAC GCCTGGTATC TTTATAGTCC TGTCGGGTTT CGCCACCTCT 5350  
 25 GACTTGAGCG TCGATTTTTG TGATGCTCGT CAGGGGGGCG GAGCCTATGG 5400  
 AAAAACGCCA GCAACGCGGC CTTTTTACGG TTCCTGGCCT TTTGCTGGCC 5450  
 30 TTTTGCTCAC ATGTTCTTTC CTGCGTTATC CCCTGATTCT GTGGATAACC 5500  
 GTATTACCGC CTTTGAGTGA GCTGATACCG CTCGCCGAG CCGAACGACC 5550  
 GAGCGCAGCG AGTCAGTGAG CGAGGAAGCG GAAGAGCGCC CAATACGCAA 5600  
 35 ACCGCTCTC CCCGCGCGTT GGCCGATTCA TTAATCCAGC TGGCAGACA 5650  
 GGTTTCCCGA CTGGAAGCG GGCAGTGAGC GCAACGCAAT TAATGTGAGT 5700  
 40 TACCTCACTC ATTAGGCACC CCAGGCTTTA CACTTTATGC TTCCGGCTCG 5750  
 TATGTTGTGT GGAATTGTGA GCGGATAACA ATTTACACA GGAAACAGCT 5800  
 ATGACCATGA TTACGAATTA ATTCGAGCTC GCCCACATT GATTATTGAC 5850  
 45 TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA 5900  
 TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG 5950  
 50 CCCAACGACC CCCGCCATT GACGTCAATA ATGACGTATG TTCCCATAGT 6000  
 AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAG TATTTACGGT 6050  
 AACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCC 6100

CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTA 6150  
 CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA 6200  
 5 TCGCTATTAC CATGGTGATG CGGTTTTGGC AGTACATCAA TGGGCGTGGA 6250  
 TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA 6300  
 TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA 6350  
 10 ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG 6400  
 GTCTATATAA GCAGAGCTCG TTTAGTGAAC CGTCAGATCG CCTGGAGACG 6450  
 15 CCATCCACGC TGTTTTGACC TCCATAGAAG ACACCGGGAC CGATCCAGCC 6500  
 TCCGCGGCCG GGAACGGTGC ATTGGAACGC GGATTCCCCG TGCCAAGAGT 6550  
 GACGTAAGTA CCGCCTATAG AGTCTATAGG CCCACCCCCT TGGCTCGTTA 6600  
 20 GAACGCGGCT ACAATTAATA CATAACCTTA TGTATCATAC ACATACGATT 6650  
 TAGGTGACAC TATAGAATAA CATCCACTTT GCCTTTCTCT CCACAGGTGT 6700  
 25 CCACTCCCAG GTCCAACTGC AGGCCATGGC GGCCATCGAT T 6741

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 631 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

35 Leu Lys Ser Pro Gln Lys Val Glu Val Asp Ile Ile Asp Asp Asn  
           1                          5                          10                          15  
 Phe Ile Leu Arg Trp Asn Arg Ser Asp Glu Ser Val Gly Asn Val  
                           20                          25                          30  
 40 Thr Phe Ser Phe Asp Tyr Gln Lys Thr Gly Met Asp Asn Trp Ile  
                           35                          40                          45  
 45 Lys Leu Ser Gly Cys Gln Asn Ile Thr Ser Thr Lys Cys Asn Phe  
                           50                          55                          60  
 Ser Ser Leu Lys Leu Asn Val Tyr Glu Glu Ile Lys Leu Arg Ile  
                           65                          70                          75  
 50 Arg Ala Glu Lys Glu Asn Thr Ser Ser Trp Tyr Glu Val Asp Ser  
                           80                          85                          90  
 Phe Thr Pro Phe Arg Lys Ala Gln Ile Gly Pro Pro Glu Val His  
                           95                          100                          105

	Leu	Glu	Ala	Glu	Asp	Lys	Ala	Ile	Val	Ile	His	Ile	Ser	Pro	Gly	110	115	120
5	Thr	Lys	Asp	Ser	Val	Met	Trp	Ala	Leu	Asp	Gly	Leu	Ser	Phe	Thr	125	130	135
	Tyr	Ser	Leu	Leu	Ile	Trp	Lys	Asn	Ser	Ser	Gly	Val	Glu	Glu	Arg	140	145	150
10	Ile	Glu	Asn	Ile	Tyr	Ser	Arg	His	Lys	Ile	Tyr	Lys	Leu	Ser	Pro	155	160	165
	Glu	Thr	Thr	Tyr	Cys	Leu	Lys	Val	Lys	Ala	Ala	Leu	Leu	Thr	Ser	170	175	180
15	Trp	Lys	Ile	Gly	Val	Tyr	Ser	Pro	Val	His	Cys	Ile	Lys	Thr	Thr	185	190	195
20	Val	Glu	Asn	Glu	Leu	Pro	Pro	Pro	Glu	Asn	Ile	Glu	Val	Ser	Val	200	205	210
	Gln	Asn	Gln	Asn	Tyr	Val	Leu	Lys	Trp	Asp	Tyr	Thr	Tyr	Ala	Asn	215	220	225
25	Met	Thr	Phe	Gln	Val	Gln	Trp	Leu	His	Ala	Phe	Leu	Lys	Arg	Asn	230	235	240
	Pro	Gly	Asn	His	Leu	Tyr	Lys	Trp	Lys	Gln	Ile	Pro	Asp	Cys	Glu	245	250	255
30	Asn	Val	Lys	Thr	Thr	Gln	Cys	Val	Phe	Pro	Gln	Asn	Val	Phe	Gln	260	265	270
35	Lys	Gly	Ile	Tyr	Leu	Leu	Arg	Val	Gln	Ala	Ser	Asp	Gly	Asn	Asn	275	280	285
	Thr	Ser	Phe	Trp	Ser	Glu	Glu	Ile	Lys	Phe	Asp	Thr	Glu	Ile	Gln	290	295	300
40	Ala	Phe	Leu	Leu	Pro	Pro	Val	Phe	Asn	Ile	Arg	Ser	Leu	Ser	Asp	305	310	315
	Ser	Phe	His	Ile	Tyr	Ile	Gly	Ala	Pro	Lys	Gln	Ser	Gly	Asn	Thr	320	325	330
45	Pro	Val	Ile	Gln	Asp	Tyr	Pro	Leu	Ile	Tyr	Glu	Ile	Ile	Phe	Trp	335	340	345
50	Glu	Asn	Thr	Ser	Asn	Ala	Glu	Arg	Lys	Ile	Ile	Glu	Lys	Lys	Thr	350	355	360
	Asp	Val	Thr	Val	Pro	Asn	Leu	Lys	Pro	Leu	Thr	Val	Tyr	Cys	Val	365	370	375

	Lys	Ala	Arg	Ala	His	Thr	Met	Asp	Glu	Lys	Leu	Asn	Lys	Ser	Ser	
					380					385					390	
5	Val	Phe	Ser	Asp	Ala	Val	Cys	Glu	Lys	Thr	Lys	Pro	Gly	Asn	Asp	
					395					400					405	
	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	
					410					415					420	
10	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	
					425					430					435	
	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	
15					440					445					450	
	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	
					455					460					465	
20	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	
					470					475					480	
	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	
					485					490					495	
25	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	
					500					505					510	
	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	
30					515					520					525	
	Gln	Pro	Arg	Glu	Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	
					530					535					540	
35	Glu	Met	Thr	Lys	Asn	Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	
					545					550					555	
	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	
					560					565					570	
40	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	Pro	Val	Leu	Asp	Ser	Asp	
					575					580					585	
	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	Val	Asp	Lys	Ser	Arg	
45					590					595					600	
	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	Val	Met	His	Glu	Ala	
					605					610					615	
50	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	Leu	Ser	Pro	Gly	
					620					625					630	
	Lys															
	631															